

# SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Method for identifying substances which positively influence inflammatory conditions of chronic inflammatory airway diseases

<130> 082\_00n

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<150> UK 0021484.1

<151> 2000-09-01

<160> 24

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<210> 10  
 <211> 972  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
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 Gly Gln Gly Ile Pro Val Ile Glu Pro Ser Val Pro Glu Leu Val Val  
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 Lys Pro Gly Ala Thr Val Thr Leu Arg Cys Val Gly Asn Gly Ser Val  
 35 40 45  
 Glu Trp Asp Gly Pro Pro Ser Pro His Trp Thr Leu Tyr Ser Asp Gly  
 50 55 60  
 Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala Thr Phe Gln Asn Thr Gly



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370	375	380
Asn Pro Gly Gly Trp Arg Ala Leu Thr Phe Glu Leu Thr Leu Arg Tyr		
385	390	395 400
Pro Pro Glu Val Ser Val Ile Trp Thr Phe Ile Asn Gly Ser Gly Thr		
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Leu Leu Cys Ala Ala Ser Gly Tyr Pro Gln Pro Asn Val Thr Trp Leu		
	420	425 430
Gln Cys Ser Gly His Thr Asp Arg Cys Asp Glu Ala Gln Val Leu Gln		
	435	440 445
Val Trp Asp Asp Pro Tyr Pro Glu Val Leu Ser Gln Glu Pro Phe His		
	450	455 460
Lys Val Thr Val Gln Ser Leu Leu Thr Val Glu Thr Leu Glu His Asn		
	465	470 475 480
Gln Thr Tyr Glu Cys Arg Ala His Asn Ser Val Gly Ser Gly Ser Trp		
	485	490 495
Ala Phe Ile Pro Ile Ser Ala Gly Ala His Thr His Pro Pro Asp Glu		
	500	505 510
Phe Leu Phe Thr Pro Val Val Val Ala Cys Met Ser Ile Met Ala Leu		
	515	520 525
Leu Leu Leu Leu Leu Leu Leu Leu Leu Tyr Lys Tyr Lys Gln Lys Pro		
	530	535 540
Lys Tyr Gln Val Arg Trp Lys Ile Ile Glu Ser Tyr Glu Gly Asn Ser		
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Tyr Thr Phe Ile Asp Pro Thr Gln Leu Pro Tyr Asn Glu Lys Trp Glu		
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Phe Pro Arg Asn Asn Leu Gln Phe Gly Lys Thr Leu Gly Ala Gly Ala		
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Phe Gly Lys Val Val Glu Ala Thr Ala Phe Gly Leu Gly Lys Glu Asp		
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Ala Val Leu Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala His Ala		
	610	615 620
Asp Glu Lys Glu Ala Leu Met Ser Glu Leu Lys Ile Met Ser His Leu		
	625	630 635 640
Gly Gln His Glu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr His Gly		
	645	650 655
Gly Pro Val Leu Val Ile Thr Glu Tyr Cys Cys Tyr Gly Asp Leu Leu		
	660	665 670
Asn Phe Leu Arg Arg Lys Ala Glu Ala Met Leu Gly Pro Ser Leu Ser		

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Glu	Lys	Lys	Tyr	Val	Arg	Arg	Asp	Ser	Gly	Phe	Ser	Ser	Gln	Gly	Val
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Asp	Thr	Tyr	Val	Glu	Met	Arg	Pro	Val	Ser	Thr	Ser	Ser	Asn	Asp	Ser
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Phe	Ser	Glu	Gln	Asp	Leu	Asp	Lys	Glu	Asp	Gly	Arg	Pro	Leu	Glu	Leu
			740					745					750		
Arg	Asp	Leu	Leu	His	Phe	Ser	Ser	Gln	Val	Ala	Gln	Gly	Met	Ala	Phe
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Leu	Ala	Ser	Lys	Asn	Cys	Ile	His	Arg	Asp	Val	Ala	Ala	Arg	Asn	Val
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Leu	Leu	Thr	Asn	Gly	His	Val	Ala	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Ala
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Arg	Asp	Ile	Met	Asn	Asp	Ser	Asn	Tyr	Ile	Val	Lys	Gly	Asn	Ala	Arg
				805					810					815	
Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp	Cys	Val	Tyr
			820					825					830		
Thr	Val	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile
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Phe	Ser	Leu	Gly	Leu	Asn	Pro	Tyr	Pro	Gly	Ile	Leu	Val	Asn	Ser	Lys
			850			855					860				
Phe	Tyr	Lys	Leu	Val	Lys	Asp	Gly	Tyr	Gln	Met	Ala	Gln	Pro	Ala	Phe
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Ala	Pro	Lys	Asn	Ile	Tyr	Ser	Ile	Met	Gln	Ala	Cys	Trp	Ala	Leu	Glu
			885						890					895	
Pro	Thr	His	Arg	Pro	Thr	Phe	Gln	Gln	Ile	Cys	Ser	Phe	Leu	Gln	Glu
			900					905					910		
Gln	Ala	Gln	Glu	Asp	Arg	Arg	Glu	Arg	Asp	Tyr	Thr	Asn	Leu	Pro	Ser
			915				920					925			
Ser	Ser	Arg	Ser	Gly	Gly	Ser	Gly	Ser	Ser	Ser	Ser	Glu	Leu	Glu	Glu
			930			935					940				
Glu	Ser	Ser	Ser	Glu	His	Leu	Thr	Cys	Cys	Glu	Gln	Gly	Asp	Ile	Ala
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Gln	Pro	Leu	Leu	Gln	Pro	Asn	Asn	Tyr	Gln	Phe	Cys				
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<210> 11  
 <211> 1696  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
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 gggctgagtc tgggccccag gacccacgtg caggcagggc acctcccaa gccaccctc 180  
 tgggctgagc caggctctgt gatcatccag ggaagtccctg tgacctcag gtgtcagggg 240  
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 cggatacaag agcctgggaa gaatggccag ttcccatcc catccatcac ctgggaacac 360  
 gcagggcggt atcactgtca gtactacagc cacaatcact catcagagta cagtgacccc 420  
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 gtggtagacct taggagggaa cgtgaccctc cagtgtgtct cacaggtggc atttgacggc 540  
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 gcccgtgggt ggtcctgggc catcttctcc gtgggccccg tgagcccagag tcgcaggtgg 660  
 tcgtacaggt gctatgctta tgactcgaac tctccctatg tgtggtctct acccagtgat 720  
 ctcttgagc tcttggtccc aggtgtttct aagaagccat cactctcagt gcagccaggt 780  
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 caagctcagc agaaccaggc tgaattccgc atgggtcctg tgacctcagc ccacgtgggg 1260  
 acctacagat gctacagctc actcagctcc aaccctacc tgctgtctct cccagtgac 1320  
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 acaatgcata ctccagcgtg gtggagcctc agggacagat ctgatgatcc caggaggctc 1560  
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<210> 12  
 <211> 466  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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 Ala Glu Pro Gly Ser Val Ile Ile Gln Gly Ser Pro Val Thr Leu Arg  
 35 40 45  
 Cys Gln Gly Ser Leu Gln Ala Glu Glu Tyr His Leu Tyr Arg Glu Asn  
 50 55 60  
 Lys Ser Ala Ser Trp Val Arg Arg Ile Gln Glu Pro Gly Lys Asn Gly  
 65 70 75 80

TOFESD 2084660

Gln	Phe	Pro	Ile	Pro	Ser	Ile	Thr	Trp	Glu	His	Ala	Gly	Arg	Tyr	His	
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Cys	Gln	Tyr	Tyr	Ser	His	Asn	His	Ser	Ser	Glu	Tyr	Ser	Asp	Pro	Leu	
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Glu	Leu	Val	Val	Thr	Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala	Leu	
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Pro	Ser	Pro	Val	Val	Thr	Leu	Gly	Gly	Asn	Val	Thr	Leu	Gln	Cys	Val	
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Ser	Gln	Val	Ala	Phe	Asp	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	Glu	Asp	
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Glu	His	Pro	Gln	Arg	Leu	Asn	Ser	His	Ser	His	Ala	Arg	Gly	Trp	Ser	
				165					170					175		
Trp	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Ser	Arg	Arg	Trp	Ser	
			180					185					190			
Tyr	Arg	Cys	Tyr	Ala	Tyr	Asp	Ser	Asn	Ser	Pro	Tyr	Val	Trp	Ser	Leu	
		195					200					205				
Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	Val	Ser	Lys	Lys	Pro	
	210					215					220					
Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Met	Val	Ala	Pro	Gly	Glu	Ser	Leu	
225					230					235					240	
Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	Arg	Phe	Val	Leu	Tyr	
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Lys	Glu	Gly	Glu	Arg	Asp	Phe	Leu	Gln	Arg	Pro	Gly	Trp	Gln	Pro	Gln	
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Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	Pro	Ser	
		275					280					285				
His	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Ser	Ala	His	Asn	Leu	Ser	Ser	Glu	
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Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly	Gln	Phe	
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Tyr	Asp	Arg	Pro	Ser	Leu	Ser	Val	Gln	Pro	Val	Pro	Thr	Val	Ala	Pro	
				325					330					335		
Gly	Lys	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Arg	Gly	Gln	Phe	His	Thr	
			340					345					350			
Phe	Leu	Leu	Thr	Lys	Glu	Gly	Ala	Gly	His	Pro	Pro	Leu	His	Leu	Arg	
		355					360					365				
Ser	Glu	His	Gln	Ala	Gln	Gln	Asn	Gln	Ala	Glu	Phe	Arg	Met	Gly	Pro	
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<210> 16  
<211> 53  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 16  
ggggaccact ttgtacaaga aagctgggtt cacattgcct gtaactcagt ctc 53

<210> 17  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 17  
agcccatagc agatggcaac 20

<210> 18  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18  
tgtactttca actttgcatc ctgg 24

<210> 19  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19  
aagccaatga caaaccggat aatccctc 28

<210> 20  
<211> 2051  
<212> DNA  
<213> Homo sapiens

<400> 20  
cgccactttg ctggagcatt cactaggcga ggcgctccat cggactcact agccgcactc 60  
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ttccgagatg acttcattgc caagggtgtg cgcgcggtgt tggggctgga gtttatcttt 180



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caaaaaaaaa a 2051

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<210> 21  
 <211> 387  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
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 Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala  
 35 40 45  
 Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile  
 50 55 60  
 Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu  
 65 70 75 80  
 Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly  
 85 90 95

004460 201000

Asp	Ile	Pro	Cys	Arg	Leu	Val	Leu	Phe	Met	Phe	Ala	Met	Asn	Arg	Gln		
			100					105					110				
Gly	Ser	Ile	Ile	Phe	Leu	Thr	Val	Val	Ala	Val	Asp	Arg	Tyr	Phe	Arg		
		115					120					125					
Val	Val	His	Pro	His	His	Ala	Leu	Asn	Lys	Ile	Ser	Asn	Trp	Thr	Ala		
		130				135					140						
Ala	Ile	Ile	Ser	Cys	Leu	Leu	Trp	Gly	Ile	Thr	Val	Gly	Leu	Thr	Val		
145					150					155					160		
His	Leu	Leu	Lys	Lys	Lys	Leu	Leu	Ile	Gln	Asn	Gly	Pro	Ala	Asn	Val		
			165						170					175			
Cys	Ile	Ser	Phe	Ser	Ile	Cys	His	Thr	Phe	Arg	Trp	His	Glu	Ala	Met		
			180					185					190				
Phe	Leu	Leu	Glu	Phe	Leu	Leu	Pro	Leu	Gly	Ile	Ile	Leu	Phe	Cys	Ser		
		195					200					205					
Ala	Arg	Ile	Ile	Trp	Ser	Leu	Arg	Gln	Arg	Gln	Met	Asp	Arg	His	Ala		
		210				215					220						
Lys	Ile	Lys	Arg	Ala	Ile	Thr	Phe	Ile	Met	Val	Val	Ala	Ile	Val	Phe		
225					230					235					240		
Val	Ile	Cys	Phe	Leu	Pro	Ser	Val	Val	Val	Arg	Ile	Arg	Ile	Phe	Trp		
			245						250					255			
Leu	Leu	His	Thr	Ser	Gly	Thr	Gln	Asn	Cys	Glu	Val	Tyr	Arg	Ser	Val		
		260						265					270				
Asp	Leu	Ala	Phe	Phe	Ile	Thr	Leu	Ser	Phe	Thr	Tyr	Met	Asn	Ser	Met		
		275					280					285					
Leu	Asp	Pro	Val	Val	Tyr	Tyr	Phe	Ser	Ser	Pro	Ser	Phe	Pro	Asn	Phe		
		290				295					300						
Phe	Ser	Thr	Leu	Ile	Asn	Arg	Cys	Leu	Gln	Arg	Lys	Met	Thr	Gly	Glu		
305					310					315					320		
Pro	Asp	Asn	Asn	Arg	Ser	Thr	Ser	Val	Glu	Leu	Thr	Gly	Asp	Pro	Asn		
			325						330					335			
Lys	Thr	Arg	Gly	Ala	Pro	Glu	Ala	Leu	Met	Ala	Asn	Ser	Gly	Glu	Pro		
			340					345					350				
Trp	Ser	Pro	Ser	Tyr	Leu	Gly	Pro	Thr	Ser	Asn	Asn	His	Ser	Lys	Lys		
		355					360					365					
Gly	His	Cys	His	Gln	Glu	Pro	Ala	Ser	Leu	Glu	Lys	Gln	Leu	Gly	Cys		
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Cys	Ile	Glu															
385																	

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 22  
agcccatagc agatggcaac 20

<210> 23  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 23  
tgtactttca actttgcatc ctgg 24

<210> 24  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 24  
aagccaatga caaaccggat aatccctc 28

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